

## AMENDMENTS TO THE CLAIMS

1. (Currently amended) A method of identifying genetic mutations that are associated with ~~ataxic neurological disease~~ adult onset cerebellar ataxia in a human subject, said method comprising:

(a) determining a first nucleic acid sequence of a human protein kinase C gamma gene from a first human subject exhibiting adult onset cerebellar ataxia;

(b) identifying a difference between the first nucleic acid sequence from the first human subject exhibiting adult onset cerebellar ataxia and SEQ ID NO:3, wherein the difference alters the amino acid sequence encoded by the human protein kinase C gamma gene; and

(c) confirming that the difference identified between the first nucleic acid sequence and SEQ ID NO:3 is a genetic mutation associated with adult onset cerebellar ataxia by co-segregation analysis comprising determining that the identified nucleic acid sequence difference is also present in a plurality of human subjects exhibiting adult onset cerebellar ataxia and is absent in a plurality of human subjects not exhibiting adult onset cerebellar ataxia.

2. (Currently amended) The method of Claim 1 wherein the first nucleic acid sequence from said first human subject is determined by amplification of ~~portions~~ at least a portion of the human protein kinase C gamma gene from genomic DNA isolated from said human subject to produce an amplified DNA and sequencing said amplified DNA.

3. (Canceled)

4. (Currently amended) The method of Claim 1 wherein said ~~co-segregation~~ co-segregation analysis comprises a method selected from the group consisting of direct

sequencing, sequencing PCR-amplified DNA, single stranded conformation analysis, allele-specific PCR and restriction fragment length polymorphism.

5. (Currently amended) The method of Claim 4 wherein said ~~co-segregation~~ co-segregation analysis comprises sequencing PCR-amplified DNA.

6. (Currently amended) The method of Claim 4 wherein said ~~co-segregation~~ co-segregation analysis comprises restriction fragment length polymorphism analysis.

7-42. (Canceled)

43. (Withdrawn – currently amended) The method of Claim ~~[[2]]~~ 1, wherein the ~~portions of nucleic acid sequence that are amplified~~ comprises at least one of first nucleic acid sequence is a coding region of the human protein kinase C gamma gene selected from the group consisting of exon 1 (nucleotides 440 to 609 of SEQ ID NO:3); exon 2 (nucleotides 1108 to 1139 of SEQ ID NO:3); exon 3 (nucleotides 2106 to 2188 of SEQ ID NO:3); exon 4 (nucleotides 7583 to 7694 of SEQ ID NO:3); exon 5 (nucleotides 7831 to 7962 of SEQ ID NO:3); exon 6 (nucleotides 9619 to 9775 of SEQ ID NO:3); exon 7 (nucleotides 10454 to 10588 of SEQ ID NO:3); exon 8 (nucleotides 10933 to 11020 of SEQ ID NO:3); exon 9 (nucleotides 11307 to 11336 of SEQ ID NO:3); exon 10 (nucleotides 15904 to 16056 of SEQ ID NO:3); exon 11 (nucleotides 16385 to 16573 of SEQ ID NO:3); exon 12 (nucleotides 18178 to 18269 of SEQ ID NO:3); exon 13 (nucleotides 18364 to 18426 of SEQ ID NO:3); exon 14 (nucleotides 18556 to 18694 of SEQ ID NO:3); exon 15 (nucleotides 21018 to 21098 of SEQ ID NO:3); exon 16 (nucleotides 22580 to 22687 of SEQ ID NO:3); exon 17 (nucleotides 24262 to 24402 of SEQ ID NO:3); ~~[[or]]~~ and exon 18 (nucleotides 24652 to 24840 of SEQ ID NO:3).

44. (Currently amended) The method of Claim ~~[[43]]~~ 1, wherein the ~~portion of SEQ ID NO:3 that is amplified~~ first nucleic acid sequence comprises exon 4 (~~nucleotides 7583 to 7694 of SEQ ID NO:3~~) of the human protein kinase C gamma gene.

45. (Currently amended) The method of Claim 1, wherein the mutation associated with adult onset cerebellar ataxia ~~neurological disease~~ is selected from the group consisting of a missense mutation, a deletion mutation, and an insertion mutation, ~~a splicing site mutation, and a mutation that results in loss of expression of the protein kinase C gamma gene encoded by SEQ ID NO:3.~~

46. (Previously presented) The method of Claim 45, wherein the mutation is a missense mutation.